# Figure 1.   BOVINE RAG2 SEQUENCE

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>

>   773 ATGTCACT ACAGATGGTA ACAGTCGGAA

>

>   801 ATAGCATAGC CTTAATTCAA CCAGGCTTCT CGTTAATGAA
TTTTGATGGG

>

>   851 CAAGTTTTCT TCTTTGGCCA AAAAGGCTGG CCCAAGAGGT
CTTGCCCCAC

>

>   901 TGGAGTTTTC CATTTTGAGG TAAAGCATAA TCATCTTAAA
CTGAAGCCTG

>

>   951 CAGTTTTCTC TAAGGATTCC TGCTACCTTC CTCCTCTTCG ATACCGGGC

>

>   1001 CACTTGCACA TTCAGCGGCC AACTTGGAGT CTGAAAAGCA
TCAGTACATC

>

>   1051 ATCCATGGAG GAAAAACACC AAACAATGAG CTTTCAGATA
AGATTTATGT

>

>   1101 GATGTCTGTT GTTTCCAAGA ACAACAAAAA AGTTACCTTT
CGCTGCACAG

>

>   1151 AGAAGGACTT GGTAGGAGAC ATTCCTGAAG GCAGATATGG
TCATTCCATT

>

>   1201 GATGTGGTGT ATAGTCGGGG GAAAAGTATG GGTGTTCTCT
TTGGAGGACG

>

>   1251 GTCATACATA CCTTCTGCCC AAAGAACCAC AGAGAAATGG
AACAGTGTAG

>

>   1301 CTGACTGCCT GCCCCATGTC TTCTTGGTGG ATTTTGAATT
TGGGTGCTCT

>

>   1351 ACGTCATACA TTCTTCCAGA ACTTCAAGAT GGACTATCTT
TTCATGTCTC

>

>   1401 CATTGCCAGA AATGATACCG TTTATATTTT AGGAGGCCAT
TCACTTGCCA

>

>   1451 ATAACATCCG CCCTGCCAAT CTGTACAGAA TAAGGGTTGA
TCTCCCCCTG

>

> 1501 GGTAGCCCAG CTGTGGAGTG CACAGTCTTG CCAGGAGGAA
TCTCTGTCTC
>
> 1551 CAGTGCAATC CTGACTCAAA TAAGCAATGA TGAATTTGTT
ATTGTTGGTG
>
> 1601 GCTATCAGCT TGAAAATCAA AAAGAATGG TCTGTAACAT
CATCTCTTTC
>
> 1651 AAGTATAACA AGATAGACAT TCTTGAGATG GAAACCCCAG
ATTGGACCCC
>
> 1701 AGATATTAAG CACAGCAAGA TATGGTTTGG AAGCAACATG
GGAAATGGAA
>
> 1751 CTGTTTTCCT CGGCATACCA GGAGACAATA AACAGGCTGT
TTCAGAAGCA
>
> 1801 TTTTACTTCT ATACATTGAA ATGTGCTGAA GACGATGTGA
ACGAAGATCA
>
> 1851 GATAACTTTG ACAAGTAGTC AGACATCAAC AGAAGACCCA
GGGGACTCCA
>
> 1901 CTCCCTTTGA AGACTCAGAA GAATTTTGCT TCAGCGCAGA
AGCAAACAGT
>
> 1951 TTCGATGGTG ATGATGAATT TGACACCTAC AATGAAGATG
ATGAGGAAGA
>
> 2001 TGAGTCTGAG ACAGGCTATT GGATTACATG CTGCCCTACT
TGTGATGTGG
>
> 2051 ATATCAATAC GTGGGTACCA TTTTATTCAA CTGAGCTCAA
CAAGCCTGCC
>
> 2101 ATGATCTATT GCTCTCATGG AGATGGACAT TGGGTCCATG
CCCAGTGTAT
>
> 2151 GGATCTGGCA GAACGCACCA CCTCATCCAT CTATCAGAAG
GAAGCAATAA
>
> 2201 ATATTAYTGT AACGAGCATG TGGAGATAG

FIG. 2 - MAP OF BOVINE RAG-2 KNOCKOUT CONSTRUCT
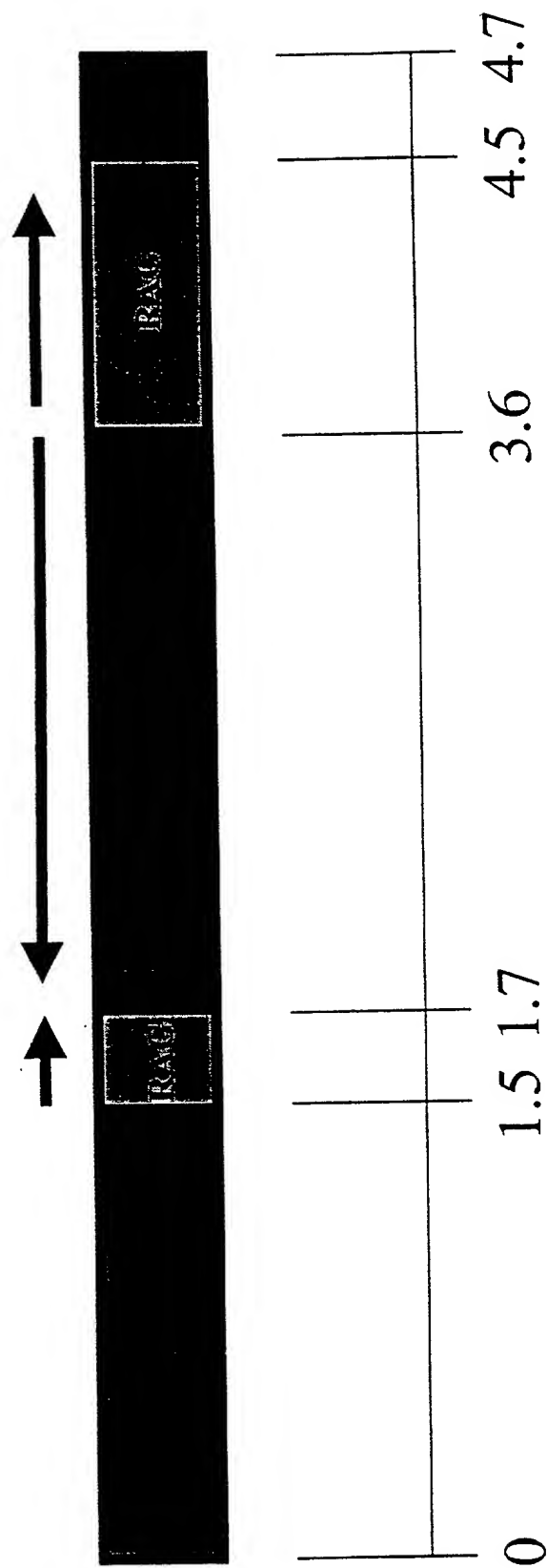
→ = TRANSCRIPTIONAL ORIENTATION

Key: Bovine 5' and 3' flanking (FL) sequences are blue; RAG-2 coding region is green
& the interrupting neomycin gene is red. Note that the transcriptional orientation
of the NEO gene is opposite to that of the RAG-2 gene.
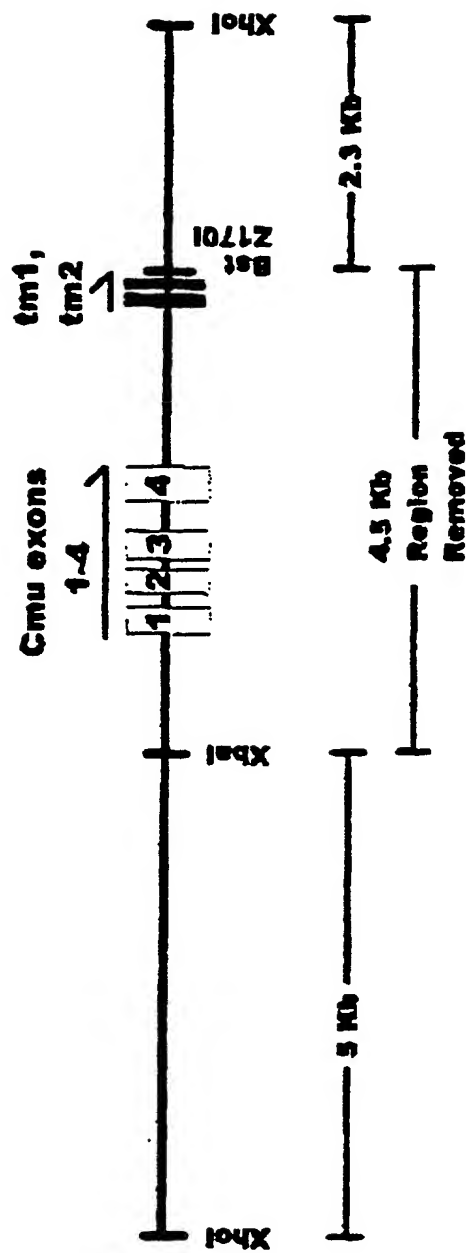
Figure 3

The 4.5 Kb region containing the exons encoding the Mu constant region and associated (transmembrane domain exons, were deleted and replaced with the loxP-flanked neomycin resistance cassette (Not I fragment)